

## SEQUENCE LISTING

<110> EVANS, Ronald FORMAN, Barry

<120> SELECTIVE MODULATORS OF PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR-GAMMA, AND METHODS FOR THE USE THEREOF

<130> SALK1470-2

<140> US 09/155,252

<141> 1998-09-21

<150> PCT/US96/05465

<151> 1996-04-18

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<170> PatentIn version 3.0

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405

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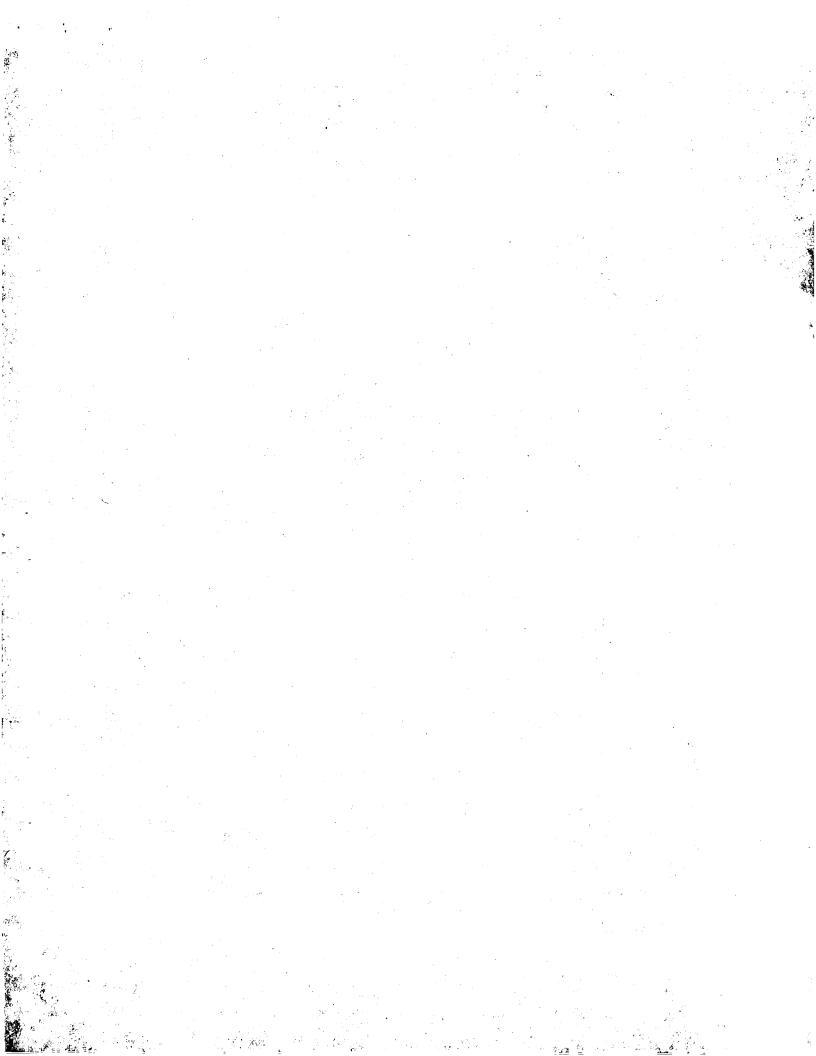
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Glu Asp Ile Pro Phe Thr Arg Ala Asp Pro Met Val Ala Asp Tyr Lys
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Tyr Asp Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro 75 80

Ala Ser Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Arg Pro 85 90 95

His Glu Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys 100 105 110

Gly Asp Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly
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Cys Lys Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp 130 135 140

Arg Cys Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys 145 150 155 160

Gln Tyr Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn 165 170 175

Ala Ile Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu 180 185 190

Ala Glu Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp 195 200 205 Leu Arg Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro Leu Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr Asp Lys Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu Asp Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys Glu Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu Ala Val Gln Glu Ile Thr Glu Tyr Ala Lys Asn Ile Pro Gly Phe Ile Asn Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn 

| Vá       | al Ly                        | s Pro                | Ile        | Glu<br>405 | Asp        | Ile        | Gln        | Asp        | Asn<br>410 | Leu        | Leu        | Gln        | Ala        | Leu<br>415 | Glu              |      |
|----------|------------------------------|----------------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------------|------|
| L€       | eu Gl                        | n Leu                | Lys<br>420 | Leu        | Asn        | His        | Pro        | Glu<br>425 | Ser        | Ser        | Gln        | Leu        | Phe<br>430 | Ala        | Lys              |      |
| Vá       | al Le                        | u Gln<br>435         |            | Met        | Thr        | Asp        | Leu<br>440 | Arg        | Gln        | Ile        | Val        | Thr<br>445 | Glu        | His        | Val              |      |
| G]       | ln Le<br>45                  | u Leu<br>0           | His        | Val        | Ile        | Lys<br>455 | Lys        | Thr        | Glu        | Thr        | Asp<br>460 | Met        | Ser        | Leu        | His              |      |
|          | ro Le<br>55                  | u Leu                | Gln        | Glu        | Ile<br>470 | Tyr        | Lys        | Asp        | Leu        | Tyr<br>475 |            |            |            |            |                  |      |
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| g        | ggaga                        | ccca                 | agct       | tgaa       | gc aa      | agcci      | cct        | g aaa      | _          | _          | _          |            | _          |            | ct atc<br>er Ile | . 55 |
| _        |                              | a gca<br>n Ala<br>10 | _          | _          |            | _          | _          |            |            | _          |            | _          | _          |            |                  | 103  |
| _        |                              | a ccg<br>s Pro       | _          | _          | _          | _          |            | _          | _          |            |            |            |            | _          | _                | 151  |
|          |                              | t ccc<br>r Pro       |            |            |            |            |            | _          | _          |            |            |            |            |            |                  | 199  |

| _ |            | - |    |   |   |   |   |   |   |   |   |   | cta<br>Leu        | _ |             | 247 |
|---|------------|---|----|---|---|---|---|---|---|---|---|---|-------------------|---|-------------|-----|
|   |            | _ | _  | _ |   | _ | _ |   | _ |   | _ | _ | tct<br>Ser<br>85  |   | -           | 295 |
| _ |            |   | -  | _ |   |   |   |   |   | _ |   | _ | aat<br>Asn        |   |             | 343 |
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|   |            | _ | _  | _ |   | _ |   | _ |   |   |   |   | tcg<br>Ser        | - |             | 439 |
| - | _          |   |    |   |   | _ | _ | _ |   | _ | _ | _ | gaa<br>Glu        |   | ccg.<br>Pro | 487 |
|   |            | _ | _  |   |   | _ |   |   | _ |   |   |   | gct<br>Ala<br>165 | _ | tag         | 535 |
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Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu 50 55 60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile 65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu 85 90 95

Phe Val Gln Asp Asn Val Asn Lys Asp Ala Val Thr Asp Arg Leu Ala 100 105 110

Ser Val Glu Thr Asp Met Pro Leu Thr Leu Arg Gln His Arg Ile Ser 115 120 125

Ala Thr Ser Ser Ser Glu Glu Ser Ser Asn Lys Gly Gln Arg Gln Leu 130 135 140

Thr Val Ser Pro Glu Phe Pro Gly Ile Arg Arg Arg Tyr Gln Ile Ser 145 150 155 160

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